Figure 1 (SEQ ID NO:1)

```
   1 ATGAAGAAAC ATCTTAAAAC AGTTGCCTTG ACCCTCACTA CAGTATCGGT AGTCACCCAC
  61 AATCAGGAAG TTTTTAGTTT AGTCAAAGAG CCAATTCTTA AACAAACTCA AGCTTCTTCA
 121 TCGATTTCTG GCGCTGACTA CGCAGAAAGT AGCGGTAAAA GCAAGTTAAA GATTAATGAA
 181 ACTTCTGGCC CTGTTGATGA TACAGTCACT GACTTATTTT CGGATAAACG TACTACTCCT
 241 GAAAAAATAA AAGATAGTCT TGCTAAAGGT CCGAGAGAAC AAGAGTTAAA GGCAGTAACA
 301 GAGAATACAG AATCAGAAAA GCAGATCACT TCTGGATCTC AACTAGAACA ATCAAAAGAG
 361 TCTCTTTCTT TAAATAAAAC AGTGCCATCA ACGTCTAATT GGGAGATTTG TGATTTTATT
 421 ACTAAGGGGA ATACCCTTGT TGGTCTTTCA AAATCAGGTG TTGAAAGTT ATCTCAAACT
 481 GATCATCTCG TATTGCCTAG TCAAGCAGGA GATGGAACTC AATTGATACA AGTAGCTAGT
 541 TTTGCTTTTA CTCCAGATAA AAAGACGGCA ATTGCAGAAT ATACCAGTAG GGCTGGAGAA
 601 AATGGGGAAA TAAGCCAACT AGATGTGGAT GGAAAGAAA TTATTAACGA AGGTGAGGTT
 661 TTTAATTCTT ATCTACTAAA GAAGGTAACA ATCCCAACTG GTTATAAACA TATTGGTCAA
 721 GATGCTTTTG TGGACAATAA GAATATTGCT GAGGTTAATC TTCCTGAAAG CCTCGAGACT
 781 ATTTCTGACT ATGCTTTTGC TCACCTAGCT TTGAAACAGA TCGATTTGCC AGATAATTTA
 841 AAAGCGATTG GAGAATTAGC TTTTTTTGAT AATCAAATTA CAGGTAAACT TTCTTTGCCA
 901 CGTCAGTTAA TGCGATTAGC AGAACGTGCT TTTAAATCAA ACCATATCAA AACAATTGAG
 961 TTTAGAGGAA ATAGTCTAAA AGTGATAGGG GAAGCTAGTT TTCAAGATAA TGATCTGAGT
1021 CAACTAATGC TACCTGACGG TCTTGAAAAA ATAGAATCAG AAGCTTTTAC AGGAAATCCA
1081 GGAGATGATC ACTACAATAA CCGTGTTGTT TTGTGGACAA AATCTGGAAA AAATCCTTCT
1141 GGTCTTGCTA CTGAAAATAC CTATGTTAAT CCTGATAAGT CACTATGGCA GGAAAGTCCT
1201 GAGATTGATT ATACTAAATG GTTAGAGGAA GATTTTACCT ATCAAAAAAA TAGTGTTACA
1261 GGTTTTTCAA ATAAAGGCTT ACAAAAAGTA AAACGTAATA AAAACTTAGA AATTCCAAAA
1321 CAGCACAATG GTGTTACTAT TACTGAAATT GGTGATAATG CTTTTCGCAA TGTTGATTTT
1381 CAAAATAAAA CTTTACGTAA ATATGATTTG GAAGAAGTAA AGCTTCCCTC AACTATTCGG
1441 AAAATAGGTG CTTTTGCTTT TCAATCTAAT AACTTGAAAT CTTTTGAAGC AAGTGACGAT
1501 TTAGAAGAGA TTAAAGAGGG AGCCTTTATG AATAATCGTA TTGAAACCTT GGAATTAAAA
1561 GATAAATTAG TTACTATTGG TGATGCGGCT TTCCATATTA ATCATATTTA TGCCATTGTT
1621 CTTCCAGAAT CTGTACAAGA AATAGGGCGT TCAGCATTTC GGCAAAATGG TGCAAATAAT
1681 CTTATTTTTA TGGGAAGTAA GGTTAAGACC TTAGGTGAGA TGGCATTTTT ATCAAATAGA
1741 CTTGAACATC TGGATCTTTC TGAGCAAAAA CAGTTAACAG AGATTCCTGT TCAAGCCTTT
1801 TCAGACAATG CCTTGAAAGA AGTATTATTA CCAGCATCAC TGAAAACGAT TCGAGAAGAA
1861 GCCTTCAAAA AGAATCATTT AAAACAACTG GAAGTGGCAT CTGCCTTGTC CCATATTGCT
1921 TTTAATGCTT TAGATGATAA TGATGGTGAT GAACAATTTG ATAATAAAGT GGTTGTTAAA
1981 ACGCATCATA ATTCCTACGC ACTAGCAGAT GGTGAGCATT TTATCGTTGA TCCAGATAAG
2041 TTATCTTCTA CAATAGTAGA CCTTGAAAAG ATTTTAAAAC TAATCGAAGG TTTAGATTAT
2101 TCTACATTAC GTCAGACTAC TCAAACTCAG TTTAGAGACA TGACTACTGC AGGTAAAGCG
2161 TTGTTGTCAA AATCTAACCT CCGACAAGCA GAAAACAAA AATTCCTTCA AGAAGCACAA
2221 TTTTTCCTTG GCCGCGTTGA TTTGGATAAA GCCATAGCTA AAGCTGAGAA GGCTTTAGTG
2281 ACCAAGAAGG CAACAAAGAA TGGTCAGTTG CTTGAAAGAA GTATTAACAA AGCGGTATTA
2341 GCTTATAATA ATAGCGCTAT TAAAAAAGCT AATGTTAAGC GCTTGGAAAA AGAGTTAGAC
2401 TTGCTAACAG GATTAGTTGA GGGAAAAGGA CCATTAGCGC AAGCTACAAT GGTACAAGGA
2461 GTTTATTTAT TAAAGACGCC TTTGCCATTG CCAGAATATT ATATCGGATT GAACGTTTAT
2521 TTTGACAAGT CTGGAAAATT GATTTATGCA CTTGATATGA GTGATACTAT GGCGAGGGA
2581 CAAAAAGACG CTTATGGTAA TCCTATATTA AATGTTGACG AGGATAATGA AGGTTATCAT
2641 GCCTTGGCAG TTGCCACTTT AGCTGATTAT GAGGGGCTCG ACATCAAAAC AATTTTAAAT
2701 AGTAAGCTTA GTCAATTAAC ATCTATTCGT CAGGTACCGA CTGCAGCCTA TCATAGAGCC
2761 GGTATTTTCC AAGCTATCCA AAATGCAGCG GCAGAAGCAG AGCAGTTATT GCCTAAACCA
2821 GGTACGCACT CTGAGAAGTC AAGCTCAAGT GAATCTGCTA ACTCTAAAGA TAGAGGATTG
2881 CAATCAAACC CAAAAACGAA TAGAGGACGA CACTCTGCAA TATTGCCTAG GACAGGGTCA
2941 AAAGGCAGCT TTGTCTATGG AATCTTAGGT TACACTAGCG TTGCTTTACT GTCACTAATA
3001 ACTGCTATAA AAAAGAAAAA ATATTAA
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1/6

Figure 2 (SEQ ID NO:2)

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  1 MKKHLKTVAL TLTTVSVVTH NQEVFSLVKE PILKQTQASS SISGADYAES SGKSKLKINE
 61 TSGPVDDTVT DLFSDKRTTP EKIKDNLAKG PREQELKAVT ENTESEKQIT SGSQLEQSKE
121 SLSLNKTVPS TSNWEICDFI TKGNTLVGLS KSGVEKLSQT DHLVLPSQAA DGTQLIQVAS
181 FAFTPDKKTA IAEYTSRAGE NGEISQLDVD GKEIINEGEV FNSYLLKKVT IPTGYKHIGQ
241 DAFVDNKNIA EVNLPESLET ISDYAFAHLA LKQIDLPDNL KAIGELAFFD NQITGKLSLP
301 RQLMRLAERA FKSNHIKTIE FRGNSLKVIG EASFQDNDLS QLMLPDGLEK IESEAFTGNP
361 GDDHYNNRVV LWTKSGKNPS GLATENTYVN PDKSLWQESP EIDYTKWLEE DFTYQKNSVT
421 GFSNKGLQKV KRNKNLEIPK QHNGVTITEI GDNAFRNVDF QNKTLRKYDL EEVKLPSTIR
481 KIGAFAFQSN NLKSFEASDD LEEIKEGAFM NNRIETLELK DKLVTIGDAA FHINHIYAIV
541 LPESVQEIGR SAFRQNGANN LIFMGSKVKT LGEMAFLSNR LEHLDLSEQK QLTEIPVQAF
601 SDNALKEVLL PASLKTIREE AFKKNHLKQL EVASALSHIA FNALDDNDGD EQFDNKVVVK
661 THHNSYALAD GEHFIVDPDK LSSTIVDLEK ILKLIEGLDY STLRQTTQTQ FRDMTTAGKA
721 LLSKSNLRQG EKQKFLQEAQ FFLGRVDLDK AIAKAEKALV TKKATKNGQL LERSINKAVL
781 AYNNSAIKKA NVKRLEKELD LLTGLVEGKG PLAQATMVQG VYLLKTPLPL PEYYIGLNVY
841 FDKSGKLIYA LDMSDTIGEG QKDAYGNPIL NVDEDNEGYH ALAVATLADY EGLDIKTILN
901 SKLSQLTSIR QVPTAAYHRA GIFQAIQNAA AEAEQLLPKP GTHSEKSSSS ESANSKDRGL
961 QSNPKTNRGR HSAILPRTGS KGSFVYGILG YTSVALLSLI TAIKKKKY*
```

Figure 3

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned..   Alignment Score = 118839
Gaps Inserted = 0   Conserved Identities = 936

Pairwise Alignment Mode: Fast
Pairwise Alignment Parameters:
    ktup = 1   Gap Penalty = 3   Top Diagonals = 5   Window Size = 5

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: blosum

Processing time: 12.9 seconds

```
Spy74_M3      1                                          DYAES    5
Spy70_M5      1                     LVKEPILKQTQASSSISGADYAES     24
Spy69_M6      1                        KQTQASSSISGADYAES         17
Spy68_M2      1                     LVKEPILKQTQASSSISGADYAES     24
Spy60_M1      1                     LVKEPILKQTQASSSISGADYAES     24
12357_M18     1                      VKEPILKQTQASSSISGADYAES     23
700294_M1     1 MKKHLKTVALTLTTVSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES  50
                                                       * * * * *


Spy74_M3      6 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    55
Spy70_M5     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    74
Spy69_M6     18 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    67
Spy68_M2     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKTVT    74
Spy60_M1     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    74
12357_M18    24 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT    73
700294_M1    51 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT   100
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *  * *


Spy74_M3     56 ENTESEKQITSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS   105
Spy70_M5     75 ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS   124
Spy69_M6     68 ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS   117
Spy68_M2     75 ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS   124
Spy60_M1     75 ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS   124
12357_M18    74 ENTESEKQINSGSQLEQSKESLSLNKRVPSTSNWEICDFITKGNTLVGLS   123
700294_M1   101 ENTESEKQITSGSQLEQSKESLSLNKTVPSTSNWEICDFITKGNTLVGLS   150
                * * * * * * * * *  * * * * * * * * * * * * * *   * * * * * * * * * * * * * * * * * * * * * * * * *


Spy74_M3    106 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   155
Spy70_M5    125 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   174
Spy69_M6    118 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   167
Spy68_M2    125 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   174
Spy60_M1    125 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   174
12357_M18   124 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   173
700294_M1   151 KSGVEKLSQTDHLVLPSQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE   200
                * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *
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Spy74_M3     156 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  205
Spy70_M5     175 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  224
Spy69_M6     168 NGEISQLDVDGKEIINEGEVFNSYLLKRVTIPTGYKHIGQDAFVDNKNIA  217
Spy68_M2     175 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  224
Spy60_M1     175 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  224
12357_M18    174 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  223
700294_M1    201 NGEISQLDVDGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA  250
                 **********************************.*.***.***.******


Spy74_M3     206 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  255
Spy70_M5     225 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  274
Spy69_M6     218 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  267
Spy68_M2     225 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  274
Spy60_M1     225 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  274
12357_M19    224 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  273
700294_M1    251 EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP  300
                 *************************************************


Spy74_M3     256 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  305
Spy70_M5     275 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  324
Spy69_M6     268 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  317
Spy68_M2     275 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  324
Spy60_M1     275 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  324
12357_M18    274 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  323
700294_M1    301 RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK  350
                 *************************************************


Spy74_M3     306 IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP  355
Spy70_M5     325 IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP  374
Spy69_M6     318 IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP  367
Spy68_M2     325 IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP  374
Spy60_M1     325 IESEAFTGNPGDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP  374
12357_M18    324 IESEAFTGNPGDDHYNNRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP  373
700294_M1    351 IESEAFTGNPGDDHYNNRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP  400
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Spy74_M3     356 EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI  405
Spy70_M5     375 EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI  424
Spy69_M6     368 EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI  417
Spy68_M2     375 EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI  424
Spy60_M1     375 EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI  424
12357_M18    374 EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKRNKNLEIPKQHNGVTITEI  423
700294_M1    401 EIDYTKWLEEDFTYQKNSVTGFSNKGLQKVKRNKNLEIPKQHNGVTITEI  450
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Spy74_M3     406 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  455
Spy70_M5     425 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  474
Spy69_M6     418 GDNAFRNVNFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  467
Spy68_M2     425 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  474
Spy60_M1     425 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  474
12357_M18    424 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  473
700294_M1    451 GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFAFQSNNLKSFEASDD  500
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Spy74_M3    456 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 505
Spy70_M5    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 524
Spy69_M6    468 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 517
Spy68_M2    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 524
Spy60_M1    475 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 524
12357_M18   474 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 523
700294_M1   501 LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR 550
                **********************************************

Spy74_M3    506 SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 555
Spy70_M5    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 574
Spy69_M6    518 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 567
Spy68_M2    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 574
Spy60_M1    525 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 574
12357_M18   524 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 574
700294_M1   551 SAFRQNGANNLIFMGSKVKTLGEMAFLSNRLEHLDLSEQKQLTEIPVQAF 600
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Spy74_M3    556 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 605
Spy70_M5    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 624
Spy69_M6    568 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 617
Spy68_M2    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 624
Spy60_M1    575 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 624
12357_M18   574 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 623
700294_M1   601 SDNALKEVLLPASLKTIREEAFKKNHLKQLEVASALSHIAFNALDDNDGD 650
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Spy74_M3    606 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLIEGLDY 655
Spy70_M5    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY 674
Spy69_M6    618 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY 667
Spy68_M2    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMIDLEKILKLIEGLDY 674
Spy60_M1    625 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY 674
12357_M18   624 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY 673
700294_M1   651 EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTIVDLEKILKLIEGLDY 700
                ********************************. .***************

Spy74_M3    656 STLRQTTQTQFRDMTTAGKALLSKSRLRQGEKQKFLQEAQFFLGRVDLDK 705
Spy70_M5    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 724
Spy69_M6    668 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 717
Spy68_M2    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 724
Spy60_M1    675 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 724
12357_M18   674 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 724
700294_M1   701 STLRQTTQTQFRDMTTAGKALLSKSNLRQGEKQKFLQEAQFFLGRVDLDK 750
                ***************************** ********************

Spy74_M3    706 AIAKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD 755
Spy70_M5    725 AIAKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD 774
Spy69_M6    718 AIAKAEKALVTKKATKNGQLLERSINKAVSAYNNSAIKKANVKRLEKELD 767
Spy68_M2    725 AIAKAEKALVTKKATKNGQLLERSINKAVSAYNNSAIKKANVKRLEKELD 767
Spy60_M1    725 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD 774
12357_M18   724 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD 774
700294_M1   751 AIAKAEKALVTKKATKNGQLLERSINKAVLAYNNSAIKKANVKRLEKELD 800
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Spy74_M3     755  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   805
Spy70_M5     775  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   824
Spy69_M6     768  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   817
Spy68_M2     775  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   824
Spy60_M1     775  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   824
12357_M18    774  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   824
700294_M1    801  LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA   850
                  +*-*++++++*+*+*+++*+**++*+**++*+*+*****+*++*+*+++*

Spy74_M3     806  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   855
Spy70_M5     825  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   874
Spy69_M6     818  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   874
Spy68_M2     825  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   867
Spy60_M1     825  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   874
12357_M18    824  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   874
700294_M1    851  LDMSDTIGEGQKDAYGNPILNVDEDNEGYHALAVATLADYEGLDIKTILN   900
                  +*-*+*+***+*+**+*+*+*+*+*+*+**+*+*+*+*+*+*+*+*+*+*+

Spy74_M3     856  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS   905
Spy70_M5     875  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKAGTHSEKSSSS   924
Spy69_M6     868  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS   917
Spy68_M2     875  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGMHSEKSSSS   924
Spy60_M1     875  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS   924
12357_M18    874  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS   923
700294_M1    901  SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS   950
                  ++++*+****+*++*+****+***+****+*****+*+**+ * +*+*+*+*

Spy74_M3     906  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      951
Spy70_M5     925  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      970
Spy69_M6     918  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      963
Spy68_M2     925  ESANSKDRGLQSHPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL      971
Spy60_M1     925  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL     971
12357_M18    924  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALL     971
700294_M1    951  ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALLSLI 1000
                  *+*+*+*+*+*+* .+*+*+*+*+*+*+*+*+*+*+*+*+*+*+*+*+**

Spy74_M3     952                 951
Spy70_M5     971                 970
Spy69_M6     964                 963
Spy68_M2     972                 971
Spy60_M1     972                 971
12357_M18    970                 969
700294_M1   1001  TAIKKKKY 1008
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